



#8

## SEQUENCE LISTING

&lt;110&gt; Attersand, Anneli

&lt;120&gt; Protein Cluster II

&lt;130&gt; 10806-156

&lt;140&gt; 10/029,359

&lt;141&gt; 2001-12-21

&lt;160&gt; 6

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 299

&lt;212&gt; DNA

&lt;213&gt; HUMAN

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (21)..(299)

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Lys Ser Trp Leu Asn Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly  
15 20 25

ttt att tta ttt tct cag cta ctt agt att ttg ttg gga gaa gag ggt 149  
Phe Ile Leu Phe Ser Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly  
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gac acc cag act aat gtt ctt cat aat gat cct cat gcg agg cat tca 197  
Asp Thr Gln Thr Asn Val Leu His Asn Asp Pro His Ala Arg His Ser  
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60 65 70 75

gat tct agc caa cgt aaa gat gag aac aca gaa atc gct gaa aac ctc	293
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Tyr	

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Val Leu His Asn Asp Pro His Ala Arg His Ser Asp Asp Asn Gly Gln	
50 55 60	
Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala Asp Ser Ser Gln Arg	
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 Thr Gly Val Thr Asp Lys Leu Tyr Gln Lys Met Lys Ile Leu Cys Trp  
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 Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile Arg  
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 Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His Asp  
 70 75 80  
 cat tat ctg gaa tac atg gat tgg ttc atg aaa gca gat gat gat ata 345  
 His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp Ile  
 85 90 95  
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 Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn Tyr  
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 aac cct gat gaa tcc act tac ttt ggg aaa aga ttt aag cac tgc aga 441  
 Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys Arg  
 115 120 125  
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 Arg Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser  
 35 40 45  
 Lys Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp  
 50 55 60  
 Arg Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His  
 65 70 75 80

Asp His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp  
85 90 95

Ile Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn  
100 105 110

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tct agc caa cat aaa gat gag aac aca gac att gct gaa aac ctc tat 97  
Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr  
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cag aaa gtt aga att ctt tgc tgg gtt atg acc ggc cct caa aac cta 145  
Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu  
35 40 45

gag aaa aag gcc aaa cac gtc aaa gct act tgg gcc cag cgt tgt aac 193  
Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn  
50 55 60

aaa gtg ttg ttt atg agt tca gaa gaa aat aaa gac ttc cct gct gtg 241  
Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val  
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gga ctg aaa acc aaa gaa ggc aga gat caa cta tac tgg aaa aca att 289  
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85 90 95

aaa gct ttt cag tat gtt cat gaa cat tat tta caa gat gct gat tgg 337  
Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp  
100 105 110

ttt ttg aaa gca gat gat gac acg tat gtc ata cta gac aat ttg agg 385

B'

Phe	Leu	Lys	Ala	Asp	Asp	Asp	Thr	Tyr	Val	Ile	Leu	Asp	Asn	Leu	Arg										
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Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu  
35 40 45

Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn  
50 55 60

Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val  
65 70 75 80

Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile  
85 90 95

Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp  
100 105 110

Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg  
115 120 125

Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg  
130 135 140

Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly  
145 150 155 160

Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys  
165 170 175

Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly  
180 185 190

Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr  
195 200 205

Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile  
210 215 220

Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr  
225 230 235 240

Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe  
245 250 255

His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr  
260 265 270

His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro  
275 280 285

Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr  
290 295 300

Lys Val Lys Leu Gly Asn Pro  
305 310

B